WHAT IS CLAIMED IS

1. A method of expression profiling, comprising:

(a) determining the expression levels of two or more nucleic acids in a test sample, wherein the ~~one~~ two or more nucleic acids is selected from the group consisting of Putative cyclin G1 interacting protein, EST (W74293), Fatty-acid –coenzyme A ligase (long-chain 3), KIAA0220, KIAA0069, Acinus, Translation initiation factor eIF1(A12/SUI1), Ornithine aminotransferase (gyrate atrophy), Insulin-like growth factor binding protein 1, Metallothionein-1H, F_1F_0-ATPase synthase *f* subunit, Ring finger protein 5, EST (H73484), XP-C repair complementing protein, Squalene epoxidase, Microsomal glutathione-S-transferase 1, Defender against cell death 1, EST (AA034268), COPII protein, KIAA0917, Corticosteroid binding globulin, Calumenin, Ubiquinol-cytochrome c reductase core protein II, SEC13 (*S. cerevisiae*)-like 1, EST (R51835), Human chromosome 3p21.1 gene sequence, Glutathione-S-transferase-like, Ribonuclease (RNase A family, 4), Transcription factor Dp-1, MAC30, Cyclin-dependent kinase 4, Multispanning membrane protein, Splicing factor (arginine/serine-rich 1), Cytochrome c-1, Lactate dehydrogenase-A, Pyrroline-5-carboxylate synthetase, Glutamate dehydrogenase, Pyruvate dehydrogenase (lipoamide) beta, Ribosomal protein S6 kinase (90kD, polypeptide 3), Acetyl-coenzyme A acetyltransferase 2, Proteasome activator subunit 3 (PA28 gamma; K_i), EST (N22016), EST (AI131502), Activating transcription factor 4, Transforming growth factor-beta type III receptor, EST (AA283846), EST (AI 310515) and EST (AA805555), wherein the numbers listed in parentheses is the GenBank accession number; and

(b) comparing the expression levels in the test sample with expression levels of the same nucleic acids in a control sample, wherein a difference in expression levels between the test and control samples is an indicator of a toxic response in the test sample.

2. The method of claim 1, wherein the determining step determines the expression levels of at least three nucleic acids selected from the group.

3. The method of claim 2, wherein the determining step determines the expression levels of at least five nucleic acids selected from the group.

4. The method of claim 3, wherein the determining step determines the expression levels of at least ten nucleic acids selected from the group.

5. The method of claim 1, wherein the group consists of Putative cyclin G1 interacting protein, EST (W74293), Fatty-acid –coenzyme A ligase (long-chain 3), KIAA0220, KIAA0069, Acinus, Translation initiation factor eIF1(A12/SUI1), Ornithine aminotransferase (gyrate atrophy), Insulin-like growth factor binding protein 1, Metallothionein-1H, F_1F_0-ATPase synthase *f* subunit, Ring finger protein 5, EST (H73484), XP-C repair complementing protein, Squalene epoxidase, Microsomal glutathione-S-transferase 1, Defender against cell death 1, EST (AA034268), COPII protein, KIAA0917, Corticosteroid binding globulin, Calumenin, Ubiquinol-cytochrome c reductase core protein II, SEC13 (*S. cerevisiae*)-like 1, EST (R51835), Human chromosome 3p21.1 gene sequence, Glutathione-S-transferase-like, Ribonuclease (RNase A family, 4), Transcription factor Dp-1, MAC30, Cyclin-dependent kinase 4, Multispanning membrane protein, Splicing factor (arginine/serine-rich 1), Cytochrome c-1, Lactate dehydrogenase-A, Pyrroline-5-carboxylate synthetase, Glutamate dehydrogenase, Pyruvate dehydrogenase (lipoamide) beta, Ribosomal protein S6 kinase (90kD, polypeptide 3), Acetyl-coenzyme A acetyltransferase 2 and Proteasome activator subunit 3 (PA28 gamma; K_i).

6. The method of claim 1, wherein the group consists of lactate dehydrogenase A, activating transcription factor 4, pyruvate dehydrogenase E1-beta subunit, transforming growth factor-beta type III receptor, EST (AI131502), EST (N22016), EST (AA283846), EST (AI310515) and EST(AA805555).

7. The method of claim 1, wherein the group consists of Cytochrome c-1, F_1F_0-ATPase synthase, Ubiquinol-cytochrome c reductase core protein II, Lactate dehydrogenase-A, Pyruvate dehydrogenase E1-beta subunit and NADH dehydrogenase subunit 2.

8. The method of claim 1, wherein the group consists of Acinus and Defender against cell death 1.

9. The method of claim 1, wherein the group consists of XP-C repair complementing protein, Glutathione-S-transferase, Metallothionein-1H, Heat shock protein 90, cAMP-dependent transcription factor ATF-4 and EST (AI148382).

10. The method of claim 1, wherein the at least one differentially expressed nucleic acid is selected from the group consisting of Lactate dehydrogenase A, Pyruvate dehydrogenase E1-beta subunit and Transforming growth factor-beta type III receptor.

11. The method of claim 1, wherein the test sample is obtained from a test cell contacted with a potential toxicant.

12. The method of claim 11, wherein the test cell is selected from the group consisting of HepG2 cells, HL60 cells, HeLa cells and MCF7 cells.

13. The method of claim 12, wherein the test cell is a HepG2 cell.

14. The method of claim 11, wherein the test cell is a population of cells.

15. The method of claim 1, wherein the determining step is performed by differential display PCR.

16. The method of claim 1, wherein the determining step is performed utilizing a probe array.

17. The method of claim 1, wherein the determining step is performed using quantitative RT-PCR.

18. The method of claim 1, further comprising:

(c) contacting a test cell capable of expressing the two or more nucleic acids with a potential toxicant; and

(d) obtaining the test sample from the test cell;

wherein the difference in expression level(s) further indicates that the potential toxicant is an actual toxicant.

19. The method of claim 1, further comprising:

(c) contacting a test cell exposed to a known toxicant and capable of expressing the two or more nucleic acids with a potential antidote;

(d) obtaining the test sample from the test cell;

wherein the absence of the difference in expression level(s) is an indication that the potential antidote is an actual antidote.

20. An isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(a) a deoxyribonucleotide sequence complementary to the full-length nucleotide sequence of SEQ ID NO:1;

(b) a ribonucleotide sequence complementary to the full-length nucleotide sequence of SEQ ID NO:1; and

(c) a nucleotide sequence complementary to the deoxyribonucleotide sequence of (a) or the ribonucleotide sequence of (b).

21. An isolated nucleic acid comprising at least 20 contiguous bases from nucleotides 153 to 224 as set forth in SEQ ID NO:1 or a complementary sequence of the same length.

22. A kit for conducting toxicity analysis, comprising:

(a) at least three polynucleotide probes that hybridize under stringent conditions to different nucleic acids selected from the group consisting of Putative cyclin G1 interacting protein, EST (W74293), Fatty-acid –coenzyme A ligase (long-chain 3), KIAA0220, KIAA0069, Acinus, Translation initiation factor eIF1(A12/SUI1), Ornithine aminotransferase (gyrate atrophy), Insulin-like growth factor binding protein 1, Metallothionein-1H, F_1F_0-ATPase synthase *f* subunit, Ring finger protein 5, EST (H73484), XP-C repair complementing protein, Squalene epoxidase, Microsomal glutathione-S-transferase 1, Defender against cell death 1, EST (AA034268), COPII protein, KIAA0917, Corticosteroid binding globulin, Calumenin, Ubiquinol-cytochrome c reductase core protein II, SEC13 (*S. cerevisiae*)-like 1, EST (R51835), Human chromosome 3p21.1 gene sequence, Glutathione-S-transferase-like, Ribonuclease (RNase A family, 4), Transcription factor Dp-1, MAC30, Cyclin-dependent kinase 4, Multispanning membrane protein, Splicing factor (arginine/serine-rich 1), Cytochrome c-1, Lactate dehydrogenase-A, Pyrroline-5-carboxylate synthetase, Glutamate dehydrogenase, Pyruvate dehydrogenase (lipoamide) beta, Ribosomal protein S6 kinase (90kD, polypeptide 3), Acetyl-coenzyme A acetyltransferase 2, Proteasome activator subunit 3 (PA28 gamma; K_i), EST (N22016), EST (AI131502), Activating transcription

factor 4, Transforming growth factor-beta type III receptor, EST (AA283846), EST (AI 310515) and EST (AA805555); and

(b) a population of cells effective for expressing the nucleic acids to which the at least three polynucleotide probes hybridize.

23. The probes of claim 22, wherein the probes are attached to a support.

24. A kit for conducting toxicity analysis, comprising at least three different primer pairs, wherein each primer pair is effective to prime the amplification of a nucleic acid segment from different nucleic acids and each primer in the primer pairs is at least 20 nucleotides long, said different nucleic acids being selected from the group consisting of Putative cyclin G1 interacting protein, EST (W74293), Fatty-acid – coenzyme A ligase (long-chain 3), KIAA0220, KIAA0069, Acinus, Translation initiation factor eIF1(A12/SUI1), Ornithine aminotransferase (gyrate atrophy), Insulin-like growth factor binding protein 1, Metallothionein-1H, F_1F_0-ATPase synthase *f* subunit, Ring finger protein 5, EST (H73484), XP-C repair complementing protein, Squalene epoxidase, Microsomal glutathione-S-transferase 1, Defender against cell death 1, EST (AA034268), COPII protein, KIAA0917, Corticosteroid binding globulin, Calumenin, Ubiquinol-cytochrome c reductase core protein II, SEC13 (*S. cerevisiae*)-like 1, EST (R51835), Human chromosome 3p21.1 gene sequence, Glutathione-S-transferase-like, Ribonuclease (RNase A family, 4), Transcription factor Dp-1, MAC30, Cyclin-dependent kinase 4, Multispanning membrane protein, Splicing factor (arginine/serine-rich 1), Cytochrome c-1, Lactate dehydrogenase-A, Pyrroline-5-carboxylate synthetase, Glutamate dehydrogenase, Pyruvate dehydrogenase (lipoamide) beta, Ribosomal protein S6 kinase (90kD, polypeptide 3), Acetyl-coenzyme A acetyltransferase 2, Proteasome activator subunit 3 (PA28 gamma; K_i), EST (N22016), EST (AI131502), Activating transcription factor 4, Transforming growth factor-beta type III receptor, EST (AA283846), EST (AI 310515) and EST (AA805555); and

(b) an enzyme effective at amplifying the segments in the presence of the appropriate nucleotides.

25. A system for expression profiling, comprising:

(a) at least three reporter constructs, each reporter construct comprising a different promoter or a response element and a heterologous reporter gene

operably linked to the promoter or response element, wherein the promoter or response element is from a gene selected from the group consisting of Putative cyclin G1 interacting protein, EST (W74293), Fatty-acid –coenzyme A ligase (long-chain 3), KIAA0220, KIAA0069, Acinus, Translation initiation factor eIF1(A12/SUI1), Ornithine aminotransferase (gyrate atrophy), Insulin-like growth factor binding protein 1, Metallothionein-1H, F_1F_0-ATPase synthase *f* subunit, Ring finger protein 5, EST (H73484), XP-C repair complementing protein, Squalene epoxidase, Microsomal glutathione-S-transferase 1, Defender against cell death 1, EST (AA034268), COPII protein, KIAA0917, Corticosteroid binding globulin, Calumenin, Ubiquinol-cytochrome c reductase core protein II, SEC13 (*S. cerevisiae*)-like 1, EST (R51835), Human chromosome 3p21.1 gene sequence, Glutathione-S-transferase-like, Ribonuclease (RNase A family, 4), Transcription factor Dp-1, MAC30, Cyclin-dependent kinase 4, Multispanning membrane protein, Splicing factor (arginine/serine-rich 1), Cytochrome c-1, Lactate dehydrogenase-A, Pyrroline-5-carboxylate synthetase, Glutamate dehydrogenase, Pyruvate dehydrogenase (lipoamide) beta, Ribosomal protein S6 kinase (90kD, polypeptide 3), Acetyl-coenzyme A acetyltransferase 2, Proteasome activator subunit 3 (PA28 gamma; K_i), EST (N22016), EST (AI131502), Activating transcription factor 4, Transforming growth factor-beta type III receptor, EST (AA283846), EST (AI 310515) and EST (AA805555); and

(b) one or more cells that harbor the at least three reporter constructs.

26. The system of claim 25, wherein the heterologous reporter gene encodes an enzyme.

27. The system of claim 26, wherein the enzyme is selected from the group consisting of β-glucuronidase, chloramphenicol acetyltransferase, luciferase, β-galactosidase and alkaline phosphatase.

28. A method of conducting expression profiling, comprising:

(a) contacting a population of test cells with a test compound, the test cells harboring at least three reporter constructs, each reporter construct comprising a different promoter or response element and a heterologous reporter gene operably linked to the promoter or response element, wherein the promoter or response element is from a gene selected from the group consisting of Putative cyclin G1 interacting protein, EST (W74293), Fatty-acid –coenzyme A ligase (long-chain 3), KIAA0220, KIAA0069,

Acinus, Translation initiation factor eIF1(A12/SUI1), Ornithine aminotransferase (gyrate atrophy), Insulin-like growth factor binding protein 1, Metallothionein-1H, F_1F_0-ATPase synthase *f* subunit, Ring finger protein 5, EST (H73484), XP-C repair complementing protein, Squalene epoxidase, Microsomal glutathione-S-transferase 1, Defender against cell death 1, EST (AA034268), COPII protein, KIAA0917, Corticosteroid binding globulin, Calumenin, Ubiquinol-cytochrome c reductase core protein II, SEC13 (*S. cerevisiae*)-like 1, EST (R51835), Human chromosome 3p21.1 gene sequence, Glutathione-S-transferase-like, Ribonuclease (RNase A family, 4), Transcription factor Dp-1, MAC30, Cyclin-dependent kinase 4, Multispanning membrane protein, Splicing factor (arginine/serine-rich 1), Cytochrome c-1, Lactate dehydrogenase-A, Pyrroline-5-carboxylate synthetase, Glutamate dehydrogenase, Pyruvate dehydrogenase (lipoamide) beta, Ribosomal protein S6 kinase (90kD, polypeptide 3), Acetyl-coenzyme A acetyltransferase 2, Proteasome activator subunit 3 (PA28 gamma; K_i), EST (N22016), EST (AI131502), Activating transcription factor 4, Transforming growth factor-beta type III receptor, EST (AA283846), EST (AI 310515) and EST (AA805555);

whereby if the test compound produces the toxic condition the promoters or response elements activate the transcription of the reporter gene to produce a detectable signal; and

(b) detecting the level of the detectable signal from the test cells; and

(c) comparing the level of the detectable signal in the test cells with the level of the detectable signal in a population of control cells under conditions identical to those for the test cells, except that the control cells are not contacted with the test compound, an increased level of signal in the test cells indicating that the test compound is a toxicant.